

SEQUENCE LISTING

<110> Cihlar, Tomas

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PC

<140> unassigned

<141> 1999-06-10

<150> 60/088,864

<151> 1998-06-11

<150> 60/132,267

<151> 1999-05-03

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 2123

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: This information
is not available.

<220>

<221> CDS

<222> (263)..(1912)

<400> 1

ttcctgccct gacccccaaa gtgaggagaa gctgcaaggg aaaagggagg gacagatcag 60
ggagaccggg gaagaaggag gacgagccaa ggaggctgct gtccccccac agagcagctc 120
ggactcagct cccgggaagc aaccagctg cggaggcaac ggcagtgtg ctctccagc 180
gaaggacagc aggcaggcag acagacagag gtctggggac tggaaggcct cagccccag 240
ccactgggct gggcctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292
Met Ala Phe Asn Asp Leu Leu Gln Gln Val
1 5 10
ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc ctc 340
Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu
15 20 25

ccc	ctg	ctc	ctg	atg	gct	tct	cac	aac	acc	ctg	cag	aac	ttc	act	gct	388
Pro	Leu	Leu	Leu	Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala	
			30					35					40			
gcc	atc	cct	acc	cac	cac	tgc	cgc	ccg	cct	gcc	gat	gcc	aac	ctc	agc	436
Ala	Ile	Pro	Thr	His	His	Cys	Arg	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser	
		45					50					55				
aag	aac	ggg	ggg	ctg	gag	gtc	tgg	ctg	ccc	cgg	gac	agg	cag	ggg	cag	484
Lys	Asn	Gly	Gly	Leu	Glu	Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln	
	60					65					70					
cct	gag	tcc	tgc	ctc	cgc	ttc	acc	tcc	ccg	cag	tgg	gga	ctg	ccc	ttt	532
Pro	Glu	Ser	Cys	Leu	Arg	Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe	
	75				80					85					90	
ctc	aat	ggc	aca	gaa	gcc	aat	ggc	aca	ggg	gcc	aca	gag	ccc	tgc	acc	580
Leu	Asn	Gly	Thr	Glu	Ala	Asn	Gly	Thr	Gly	Ala	Thr	Glu	Pro	Cys	Thr	
			95						100					105		
gat	ggc	tgg	atc	tat	gac	aac	agc	acc	ttc	cca	tct	acc	atc	gtg	act	628
Asp	Gly	Trp	Ile	Tyr	Asp	Asn	Ser	Thr	Phe	Pro	Ser	Thr	Ile	Val	Thr	
			110					115					120			
gag	tgg	gac	ctt	gtg	tgc	tct	cac	agg	gcc	cta	cgc	cag	ctg	gcc	cag	676
Glu	Trp	Asp	Leu	Val	Cys	Ser	His	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln	
		125					130					135				
tcc	ttg	tac	atg	gtg	ggg	gtg	ctg	ctc	gga	gcc	atg	gtg	ttc	ggc	tac	724
Ser	Leu	Tyr	Met	Val	Gly	Val	Leu	Leu	Gly	Ala	Met	Val	Phe	Gly	Tyr	
	140					145					150					
ctt	gca	gac	agg	cta	ggc	cgc	cgg	aag	gta	ctc	atc	ttg	aac	tac	ctg	772
Leu	Ala	Asp	Arg	Leu	Gly	Arg	Arg	Lys	Val	Leu	Ile	Leu	Asn	Tyr	Leu	
	155				160					165					170	
cag	aca	gct	gtg	tca	ggg	acc	tgc	gca	gcc	ttc	gca	ccc	aac	ttc	ccc	820
Gln	Thr	Ala	Val	Ser	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Asn	Phe	Pro	
				175				180						185		
atc	tac	tgc	gcc	ttc	cgg	ctc	ctc	tgc	ggc	atg	gct	ctg	gct	ggc	atc	868
Ile	Tyr	Cys	Ala	Phe	Arg	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Gly	Ile	
			190					195					200			
tcc	ctc	aac	tgc	atg	aca	ctg	aat	gtg	gag	tgg	atg	ccc	att	cac	aca	916
Ser	Leu	Asn	Cys	Met	Thr	Leu	Asn	Val	Glu	Trp	Met	Pro	Ile	His	Thr	
		205					210					215				
cgg	gcc	tgc	gtg	ggc	acc	ttg	att	ggc	tat	gtc	tac	agc	ctg	ggc	cag	964
Arg	Ala	Cys	Val	Gly	Thr	Leu	Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln	
	220					225					230					

ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac ctg	1012
Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His Leu	
235 240 245 250	
cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc tgg	1060
Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp	
255 260 265	
ttc ttc att gag tgc gcc cgc tgg cac tcc tcc tcc ggg agg ctg gac	1108
Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu Asp	
270 275 280	
ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag cgg	1156
Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg	
285 290 295	
gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg cag	1204
Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln	
300 305 310	
aag gag ctg acc atg ggc aaa ggc cag gca tgc gcc atg gag ctg ctg	1252
Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu Leu	
315 320 325 330	
cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg tgg	1300
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu Trp	
335 340 345	
ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag ggc	1348
Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly	
350 355 360	
ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg gac	1396
Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val Asp	
365 370 375	
ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt cgc	1444
Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly Arg	
380 385 390	
cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc ctg	1492
Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu	
395 400 405 410	
ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct ctt	1540
Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser Leu	
415 420 425	
gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc ttc	1588
Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe	
430 435 440	

ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc atg 1636
Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly Met
445 450 455

gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca ctg 1684
Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro Leu
460 465 470

gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac 1732
Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr
475 480 485 490

ggc gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca gag 1780
Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu
495 500 505

acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg 1828
Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg
510 515 520

aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc 1876
Lys Gly Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val
525 530 535

cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga 1922
Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu
540 545 550

gaagggggcct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982

caaggaggag gaagaggaaa tggtgaccca agtgtggggg ttgtggttca ggaaagcatc 2042

ttcccagggg tccacctccc ttataaaacc ccaccagaac cacatcatta aaagggtttga 2102

ctgcgaaaaa aaaaaaaaaa a 2123

<210> 2
<211> 550
<212> PRT
<213> Unknown

<400> 2
Met Ala Phe Asn Asp Leu Leu Gln Gln Val Gly Gly Val Gly Arg Phe
1 5 10 15

Gln Gln Ile Gln Val Thr Leu Val Val Leu Pro Leu Leu Leu Met Ala
20 25 30

Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
35 40 45

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
 50 55 60
 Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
 65 70 75 80
 Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
 85 90 95
 Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
 100 105 110
 Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
 115 120 125
 Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
 130 135 140
 Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
 145 150 155 160
 Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
 165 170 175
 Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
 180 185 190
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
 195 200 205
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
 210 215 220
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
 225 230 235 240
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
 245 250 255
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
 260 265 270
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
 275 280 285
 Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
 290 295 300
 Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly
 305 310 315 320

Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg
 325 330 335
 His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala
 340 345 350
 Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr
 355 360 365
 Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val
 370 375 380
 Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala
 385 390 395 400
 Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro
 405 410 415
 Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly
 420 425 430
 Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu
 435 440 445
 Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met
 450 455 460
 Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu
 465 470 475 480
 Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala
 485 490 495
 Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu
 500 505 510
 Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg
 515 520 525
 Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala Ser Ala
 530 535 540
 Gln Glu Lys Asn Gly Leu
 545 550

<210> 3

<211> 77

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: This information is not available.

```
<400> 3
accgtctaga attcttttta tttttaattt tctttcaa at acgtccacca tggccttta 60
tgacctctg cagcagg                                     77
```

```
<210> 4
<211> 51
<212> DNA
<213> Unknown
```

```
<220>
<223> Description of Unknown Organism:This information
is not available.
```

<400> 4
tactcacgtg gatcctgac agacgtctgt aggaccttcc ctccctttag g 51

<210>	5
<211>	9
<212>	DNA
<213>	Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

```
<400> 5
ccaccatgg
```

```
<210> 6
<211> 25
<212> DNA
<213> Unknown
```

```
<220>
<223> Description of Unknown Organism:This information
is not available.
```

```
<400> 6
cccgctggca ctctctctcc gggag                25
```

```
<210> 7
<211> 26
<212> DNA
<213> Unknown
```

<220>
<223> Description of Unknown Organism: This information
is not available.

<400> 7
gtagagctcg gcagtcacgc tcacca 26

<210> 8
<211> 24
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

<400> 8
ccagcgctgt cactgtcctc ctgc 24

<210> 9
<211> 29
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

<400> 9
aaccaccaca cttgggtcac catttcctc 29

<210> 10
<211> 14
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

<400> 10
Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg
1 5 10

10086916-022000